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while the level of methylation on Lys4

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the same protein is used to separate enhancers (H3K4me1-enriched)

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promoters (H3K4me3-enriched). However, as very enhancers

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remains largely unknown.

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Active enhancers and promoters tend to be depleted of histone proteins and contain accessible DNA on which various transcription factors and cofactors bind \cite{}. These regulatory regions also tend to be flanked by nucleosomes that contain histone proteins with certain characteristic post-translational modifications \cite{}. These characteristics lead to an enriched “double peak” signal containing troughs on regulatory regions within different ChIP-Seq experiments for various histone modifications such as acetylation on H3K27 and methylations on H3K4 \cite{}.

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factor (TAF) 1, TAF7, GTF2F1, and TATA-box binding protein (TBP) than enhancers. SP1, SP2, and SP4 are promoter-associated transcription

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on active promoters. On the other hand, a larger proportion of the NANOG, POU5F1, and BCL11 binding sites are found on enhancers than on

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. These transcription factors are known to play key roles in stem-cell pluripotency and are required for the propagation of undifferentiated embryonic stem-cells in culture. As expected, repressors such as SUZ12, ZNF274, and FOSL1 have very few ChIP-seq peaks on active promoters and enhancers.

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then analyzed the co-association of pairs of TRFs by analyzing the overlap between peaks of same TRF on enhancers and promoters separately. To do this, we calculated the proportion of enhancers (or promoters) that contain a ChIP-seq peak for a particular TRF also contain a ChIP-seq peak for a second TRF. While a number of general trends regarding TRF co-association is captured by these analyses, we observe that the co-association patterns of TRFs at promoters are distinct from its co-association patterns at enhancers. These TRF co-associations could lead to mechanistic insights of cooperativity between TFs.

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For example, similar to a previous study \cite{}, CTCF and ZNF143 may function cooperatively as they are observed to co-occur frequently at distal regulatory regions in this study.

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Similarly, SP4 and RXRA co-occur quite often on enhancers and promoters.